

58049-00019.ST25

SEQUENCE LISTING

<110> Republic of National Fisheries Research and Development Institute

KIM, Young Ok
 KIM, Han Woo
 LEE, Jeong Ho
 KIM, Kyung Kil
 LEE, Jong Yun
 KONG, In Soo

<120> Phytase produced from Citrobacter braakii

<130> 58049-00019

<150> PCT/KR2004/000680

<151> 2004-03-25

<150> KR 10-2003-0018573

<151> 2003-03-25

<160> 8

<170> KopatentIn 1.71

<210> 1

<211> 1481

<212> DNA

<213> Citrobacter braakii YH-15

<220>

<221> MISC_FEATURE

<222> (1134)..(1134)

<223> n can be a, c, g or t

<400> 1

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ggaaactgcc cgatggaggg ggataactac tggaaacggt agctaatacc gcataacgtc 180

gcaagaccaa agagggggac cttcgggcct cttgccatcg gatgtgccca gatgggattta 240

gctagtaggt ggggtaacgg ctcacctagg cgacgatccc tagctggtct gagaggatga 300

ccagccacac tggaaactgag acacggtcca gactcctacg ggaggcagca gtggggaaata 360

ttgcacaatg ggcgcaagcc tcatgcagcc atgccgcgtg tatgaagaag gccttcgggt 420

tgtaaagtac ttgcagcggag gaggaaggtg ttgtggtaa taaccgcagc aattgacgtt 480

actcgccagaa gaagcaccgg ctaactccgt gccagcagcc gcggtaatac ggagggtgca 540

agcgtaatc ggaattactg ggcgtaaagc gcacgcaggc ggtctgtcaa gtcggatgtg 600

aaatccccgg gctcaacctg ggaactgcat ccgaaactgg caggctagag tctttagag 660

ggggtagaa ttccaggtgt agcggtaaa tgcgtagaga tctggaggaa taccgggtggc 720

gaaggcggcc ccctggacaa agactgacgc tcaggtgcga aagcgtgggg agcaaacagg 780

attagataacc ctggtagtcc acgccgtaaa cgatgtcgac ttggaggttgc tgccctttag 840

gcgtggcttc cggagctaac gcgttaagtc gaccgcctgg ggagtacggc cgcaaggta 900

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<210> 2
<211> 10
<212> PRT
<213> Citrobacter braakii YH-15

<400> 2
Glu Glu Gln Asn Gly Met Lys Leu Glu Arg
1 5 10

<210> 3
<211> 12
<212> PRT
<213> Escherichia coli

<400> 3
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<210> 4
<211> 15
<212> PRT
<213> Aspergillus ficuum

<400> 4
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1 5 10 15

<210> 5
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<212> PRT
<213> Bacillus sp.

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa can be any natural amino acid

<400> 5

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Ser Asp Pro Tyr His Phe Thr Val Asn Ala Ala Xaa Glu Thr Glu
1 5 10 15

<210> 6
<211> 1302
<212> DNA
<213> Citrobacter braakii YH-15

<220>
<221> gene
<222> (1)..(1302)
<223> phytase gene

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gtaagagcac ctacgaagtt cactccaata atgaaagatg tcacacccga ccaatggcca 180
caatgggatg tgccgttagg atggctaacg cctcgtgggg gagaacttgt ttctgaatta 240
ggtcagtatc aacgtttatg gttcacaagg aaaggcttgt tgaataatca aacgtgccca 300
tctccagggc aggttgctgt tattgcagac acggatcaac gcacccgtaa aacgggttag 360
gcgtttctgg ctgggttagc accaaaatgt caaattcaag tgcattatca gaaggatgaa 420
aaaaaaaatg atccctttt taatccgtt aaaaatggga aatgttcgtt taacacattt 480
aaggtaaaa acgctattct ggaacgggccc ggaggaaata ttgaactgtt tacccaaacgc 540
tatcaatctt catttcggac cctggaaaat gttttaaatt tctcacaatc ggagacatgt 600
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gtaactcctg acaacgtatc attacctggt gcctggagtc tttcttccac gctgacttag 720
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aaaaaagaat ggagagattt gttaagtctg cataacgctc agtttgcattt tttgcaaaga 840
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ttgacaaatg gtacaacaga aaacaggtat ggcataaaaat tacccgtatc tctgttgc 960
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agaaccagtg ataatacgga ttgggttcag gtttcatttgc tttatcagac gctgagagat 1140
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attaaggaaa ttgcgtgcc agagtgtgca gttacggaaat aa 1302

<210> 7
<211> 433
<212> PRT

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<213> Citrobacter braakii YH-15

<220>

<221> PEPTIDE
<222> (1)..(433)
<223> phytase

<400> 7

Met Ser Thr Phe Ile Ile Arg Leu Leu Ile Phe Ser Leu Leu Cys Gly
1 5 10 15Ser Phe Ser Ile His Ala Glu Glu Gln Asn Gly Met Lys Leu Glu Arg
20 25 30Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Phe Thr
35 40 45Pro Ile Met Lys Asp Val Thr Pro Asp Gln Trp Pro Gln Trp Asp Val
50 55 60Pro Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Val Ser Glu Leu
65 70 75 80Gly Gln Tyr Gln Arg Leu Trp Phe Thr Ser Lys Gly Leu Leu Asn Asn
85 90 95Gln Thr Cys Pro Ser Pro Gly Gln Val Ala Val Ile Ala Asp Thr Asp
100 105 110Gln Arg Thr Arg Lys Thr Gly Glu Ala Phe Leu Ala Gly Leu Ala Pro
115 120 125Lys Cys Gln Ile Gln Val His Tyr Gln Lys Asp Glu Glu Lys Asn Asp
130 135 140Pro Leu Phe Asn Pro Val Lys Met Gly Lys Cys Ser Phe Asn Thr Leu
145 150 155 160Lys Val Lys Asn Ala Ile Leu Glu Arg Ala Gly Gly Asn Ile Glu Leu
165 170 175Tyr Thr Gln Arg Tyr Gln Ser Ser Phe Arg Thr Leu Glu Asn Val Leu
180 185 190Asn Phe Ser Gln Ser Glu Thr Cys Lys Thr Thr Glu Lys Ser Thr Lys
195 200 205Cys Thr Leu Pro Glu Ala Leu Pro Ser Glu Phe Lys Val Thr Pro Asp
210 215 220Asn Val Ser Leu Pro Gly Ala Trp Ser Leu Ser Ser Thr Leu Thr Glu
225 230 235 240Ile Phe Leu Leu Gln Glu Ala Gln Gly Met Pro Gln Val Ala Trp Gly
245 250 255Arg Ile Thr Gly Glu Lys Glu Trp Arg Asp Leu Leu Ser Leu His Asn
260 265 270Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
275 280 285

Ala Thr Pro Leu Leu Asp Met Ile Asp Thr Ala Leu Leu Thr Asn Gly

290

295

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300

Thr Thr Glu Asn Arg Tyr Gly Ile Lys Leu Pro Val Ser Leu Leu Phe
305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Ser Gly Ala Leu Asp
325 330 335

Leu Lys Trp Ser Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Lys Trp Lys Arg Thr Ser Asp Asn Thr Asp Trp
355 360 365

Val Gln Val Ser Phe Val Tyr Gln Thr Leu Arg Asp Met Arg Asp Ile
370 375 380

Gln Pro Leu Ser Leu Glu Lys Pro Ala Gly Lys Val Asp Leu Lys Leu
385 390 395 400

Ile Ala Cys Glu Glu Lys Asn Ser Gln Gly Met Cys Ser Leu Lys Ser
405 410 415

Phe Ser Arg Leu Ile Lys Glu Ile Arg Val Pro Glu Cys Ala Val Thr
420 425 430

Glu

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for the detection of phytase gene

<400> 8
gargarcaga ayggyatgaa actggarcgy 30